SEQUENCE LISTING

<110> Houghton, Michael

<120> HCV FUSION PROTEINS WITH MODIFIED NS3 DOMAINS

<130> PP19545.003 (2300-19545)

<150> 60/394,510
<151> 2002-07-08

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<151> 2000-11-22

<150> 60/167,502
<151> 1999-11-24

<160> 8

<170> PatentIn version 3.2

<210> 1
<211> 9
<212> PRT
<213> Artificial

<220>
<223> epitope recognized by a Tcell receptor

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His Glu Tyr Pro Val Gly Ser Gln Leu
1   5

<210> 2
<211> 15
<212> PRT
<213> Artificial

<220>
<223> epitope recognized by a Tcell receptor

<400> 2

Ala Glu Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly
1   5   10   15

<210> 3
<211> 546
<212> DNA
<213> Artificial

<220>
<223> DNA sequence of a representative native, unmodified NS3 protease
domain

<400> 3

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atg gcg ccc atc acg gcg tac gcc cag cag aca agg ggc ctc cta ggg    48
Met Ala Pro Ile Thr Ala Tyr Ala Gln Gln Thr Arg Gly Leu Leu Gly
 1               5                  10                  15

tgc ata atc acc agc cta act ggc cgg gac aaa aac caa gtg gag ggt    96
Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
                20                  25                  30

gag gtc cag att gtg tca act gct gcc caa acc ttc ctg gca acg tgc    144
Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys
            35                  40                  45

atc aat ggg gtg tgc tgg act gtc tac cac ggg gcc gga acg agg acc    192
Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
        50                  55                  60

atc gcg tca ccc aag ggt cct gtc atc cag atg tat acc aat gta gac    240
Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
 65                  70                  75                  80

caa gac ctt gtg ggc tgg ccc gct ccg caa ggt agc cga tca ttg aca    288
Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
                85                  90                  95

ccc tgc act tgc ggc tcc tcg gac ctt tac ctg gtc acg agg cac gcc    336
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
                100                 105                 110

gat gtc att ccc gtg cgc cgg cgg ggt gat agc agg ggc agc ctg ctg    384
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
            115                 120                 125

tcg ccc cgg ccc att tcc tac ttg aaa ggc tcc tcg ggg ggt ccg ctg    432
Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
        130                 135                 140

ttg tgc ccc gcg ggg cac gcc gtg ggc ata ttt agg gcc gcg gtg tgc    480
Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
145                 150                 155                 160

acc cgt gga gtg gct aag gcg gtg gac ttt atc cct gtg gag aac cta    528
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu
                165                 170                 175

gag aca acc atg agg tcc                                            546
Glu Thr Thr Met Arg Ser
                180
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<210> 4

2

<211> 182
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of a representative native unmodified NS3
      protease domain

<400> 4

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Met Ala Pro Ile Thr Ala Tyr Ala Gln Gln Thr Arg Gly Leu Leu Gly
 1               5                  10                  15

Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
            20                  25                  30

Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys
        35                  40                  45

Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
    50                  55                  60

Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
 65                  70                  75                  80

Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
            85                  90                  95

Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
            100                 105                 110

Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
            115                 120                 125

Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
    130                 135                 140

Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
145                 150                 155                 160

Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu
                165                 170                 175

Glu Thr Thr Met Arg Ser
                180
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<210> 5
<211> 5676
<212> DNA
<213> Artificial

<220>
<223> DNA sequence of a representative modified fusion protein, with
      the NS3 protease domain deleted from the N-terminus and including
      amino acids 1-121 of Core on the C-terminus

3

<400> 5

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atg gct gca tat gca gct cag ggc tat aag gtg cta gta ctc aac ccc    48
Met Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro
 1               5                  10                  15

tct gtt gct gca aca ctg ggc ttt ggt gct tac atg tcc aag gct cat    96
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His
            20                  25                  30

ggg atc gat cct aac atc agg acc ggg gtg aga aca att acc act ggc   144
Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly
            35                  40                  45

agc ccc atc acg tac tcc acc tac ggc aag ttc ctt gcc gac ggc ggg   192
Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly
        50                  55                  60

tgc tcg ggg ggc gct tat gac ata ata att tgt gac gag tgc cac tcc   240
Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser
 65                  70                  75                  80

acg gat gcc aca tcc atc ttg ggc att ggc act gtc ctt gac caa gca   288
Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala
                85                  90                  95

gag act gcg ggg gcg aga ctg gtt gtg ctc gcc acc gcc acc cct ccg   336
Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro
            100                 105                 110

ggc tcc gtc act gtg ccc cat ccc aac atc gag gag gtt gct ctg tcc   384
Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser
            115                 120                 125

acc acc gga gag atc cct ttt tac ggc aag gct atc ccc ctc gaa gta   432
Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val
        130                 135                 140

atc aag ggg ggg aga cat ctc atc ttc tgt cat tca aag aag aag tgc   480
Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys
145                 150                 155                 160

gac gaa ctc gcc gca aag ctg gtc gca ttg ggc atc aat gcc gtg gcc   528
Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala
                165                 170                 175

tac tac cgc ggt ctt gac gtg tcc gtc atc ccg acc agc ggc gat gtt   576
Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val
            180                 185                 190

gtc gtc gtg gca acc gat gcc ctc atg acc ggc tat acc ggc gac ttc   624
Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe
            195                 200                 205

gac tcg gtg ata gac tgc aat acg tgt gtc acc cag aca gtc gat ttc   672
Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe
        210                 215                 220
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4

```
agc ctt gac cct acc ttc acc att gag aca atc acg ctc ccc caa gat    720
Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Ile Thr Leu Pro Gln Asp
225             230             235             240

gct gtc tcc cgc act caa cgt cgg ggc agg act ggc agg ggg aag cca    768
Ala Val Ser Arg Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro
            245             250             255

ggc atc tac aga ttt gtg gca ccg ggg gag cgc ccc tcc ggc atg ttc    816
Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe
            260             265             270

gac tcg tcc gtc ctc tgt gag tgc tat gac gca ggc tgt gct tgg tat    864
Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr
            275             280             285

gag ctc acg ccc gcc gag act aca gtt agg cta cga gcg tac atg aac    912
Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn
            290             295             300

acc ccg ggg ctt ccc gtg tgc cag gac cat ctt gaa ttt tgg gag ggc    960
Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly
305             310             315             320

gtc ttt aca ggc ctc act cat ata gat gcc cac ttt cta tcc cag aca    1008
Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr
            325             330             335

aag cag agt ggg gag aac ctt cct tac ctg gta gcg tac caa gcc acc    1056
Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu Val Ala Tyr Gln Ala Thr
            340             345             350

gtg tgc gct agg gct caa gcc cct ccc cca tcg tgg gac cag atg tgg    1104
Val Cys Ala Arg Ala Gln Ala Pro Pro Ser Trp Asp Gln Met Trp
            355             360             365

aag tgt ttg att cgc ctc aag ccc acc ctc cat ggg cca aca ccc ctg    1152
Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu
370             375             380

cta tac aga ctg ggc gct gtt cag aat gaa atc acc ctg acg cac cca    1200
Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Ile Thr Leu Thr His Pro
385             390             395             400

gtc acc aaa tac atc atg aca tgc atg tcg gcc gac ctg gag gtc gtc    1248
Val Thr Lys Tyr Ile Met Thr Cys Met Ser Ala Asp Leu Glu Val Val
            405             410             415

acg agc acc tgg gtg ctc gtt ggc ggc gtc ctg gct gct ttg gcc gcg    1296
Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala
            420             425             430

tat tgc ctg tca aca ggc tgc gtg gtc ata gtg ggc agg gtc gtc ttg    1344
Tyr Cys Leu Ser Thr Gly Cys Val Val Ile Val Gly Arg Val Val Leu
            435             440             445
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5

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tcc ggg aag ccg gca atc ata cct gac agg gaa gtc ctc tac cga gag    1392
Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu
    450             455             460

ttc gat gag atg gaa gag tgc tct cag cac tta ccg tac atc gag caa    1440
Phe Asp Glu Met Glu Glu Cys Ser Gln His Leu Pro Tyr Ile Glu Gln
465             470             475             480

ggg atg atg ctc gcc gag cag ttc aag cag aag gcc ctc ggc ctc ctg    1488
Gly Met Met Leu Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu
            485             490             495

cag acc gcg tcc cgt cag gca gag gtt atc gcc cct gct gtc cag acc    1536
Gln Thr Ala Ser Arg Gln Ala Glu Val Ile Ala Pro Ala Val Gln Thr
            500             505             510

aac tgg caa aaa ctc gag acc ttc tgg gcg aag cat atg tgg aac ttc    1584
Asn Trp Gln Lys Leu Glu Thr Phe Trp Ala Lys His Met Trp Asn Phe
        515             520             525

atc agt ggg ata caa tac ttg gcg ggc ttg tca acg ctg cct ggt aac    1632
Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn
    530             535             540

ccc gcc att gct tca ttg atg gct ttt aca gct gct gtc acc agc cca    1680
Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ala Val Thr Ser Pro
545             550             555             560

cta acc act agc caa acc ctc ctc ttc aac ata ttg ggg ggg tgg gtg    1728
Leu Thr Thr Ser Gln Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val
            565             570             575

gct gcc cag ctc gcc gcc ccc ggt gcc gct act gcc ttt gtg ggc gct    1776
Ala Ala Gln Leu Ala Ala Pro Gly Ala Ala Thr Ala Phe Val Gly Ala
            580             585             590

ggc tta gct ggc gcc gcc atc ggc agt gtt gga ctg ggg aag gtc ctc    1824
Gly Leu Ala Gly Ala Ala Ile Gly Ser Val Gly Leu Gly Lys Val Leu
        595             600             605

ata gac atc ctt gca ggg tat ggc gcg ggc gtg gcg gga gct ctt gtg    1872
Ile Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu Val
        610             615             620

gca ttc aag atc atg agc ggt gag gtc ccc tcc acg gag gac ctg gtc    1920
Ala Phe Lys Ile Met Ser Gly Glu Val Pro Ser Thr Glu Asp Leu Val
625             630             635             640

aat cta ctg ccc gcc atc ctc tcg ccc gga gcc ctc gta gtc ggc gtg    1968
Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val
            645             650             655

gtc tgt gca gca ata ctg cgc cgg cac gtt ggc ccg ggc gag ggg gca    2016
Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala
            660             665             670

gtg cag tgg atg aac cgg ctg ata gcc ttc gcc tcc cgg ggg aac cat    2064
```

6

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Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His
        675              680              685

gtt tcc ccc acg cac tac gtg ccg gag agc gat gca gct gcc cgc gtc    2112
Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val
        690              695              700

act gcc ata ctc agc agc ctc act gta acc cag ctc ctg agg cga ctg    2160
Thr Ala Ile Leu Ser Ser Leu Thr Val Thr Gln Leu Leu Arg Arg Leu
705              710              715              720

cac cag tgg ata agc tcg gag tgt acc act cca tgc tcc ggt tcc tgg    2208
His Gln Trp Ile Ser Ser Glu Cys Thr Thr Pro Cys Ser Gly Ser Trp
                725              730              735

cta agg gac atc tgg gac tgg ata tgc gag gtg ttg agc gac ttt aag    2256
Leu Arg Asp Ile Trp Asp Trp Ile Cys Glu Val Leu Ser Asp Phe Lys
            740              745              750

acc tgg cta aaa gct aag ctc atg cca cag ctg cct ggg atc ccc ttt    2304
Thr Trp Leu Lys Ala Lys Leu Met Pro Gln Leu Pro Gly Ile Pro Phe
        755              760              765

gtg tcc tgc cag cgc ggg tat aag ggg gtc tgg cga ggg gac ggc atc    2352
Val Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile
        770              775              780

atg cac act cgc tgc cac tgt gga gct gag atc act gga cat gtc aaa    2400
Met His Thr Arg Cys His Cys Gly Ala Glu Ile Thr Gly His Val Lys
785              790              795              800

aac ggg acg atg agg atc gtc ggt cct agg acc tgc agg aac atg tgg    2448
Asn Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg Asn Met Trp
                805              810              815

agt ggg acc ttc ccc att aat gcc tac acc acg ggc ccc tgt acc ccc    2496
Ser Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro
                820              825              830

ctt cct gcg ccg aac tac acg ttc gcg cta tgg agg gtg tct gca gag    2544
Leu Pro Ala Pro Asn Tyr Thr Phe Ala Leu Trp Arg Val Ser Ala Glu
        835              840              845

gaa tac gtg gag ata agg cag gtg ggg gac ttc cac tac gtg acg ggt    2592
Glu Tyr Val Glu Ile Arg Gln Val Gly Asp Phe His Tyr Val Thr Gly
        850              855              860

atg act act gac aat ctt aaa tgc ccg tgc cag gtc cca tcg ccc gaa    2640
Met Thr Thr Asp Asn Leu Lys Cys Pro Cys Gln Val Pro Ser Pro Glu
865              870              875              880

ttt ttc aca gaa ttg gac ggg gtg cgc cta cat agg ttt gcg ccc ccc    2688
Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Phe Ala Pro Pro
                885              890              895

tgc aag ccc ttg ctg cgg gag gag gta tca ttc aga gta gga ctc cac    2736
Cys Lys Pro Leu Leu Arg Glu Glu Val Ser Phe Arg Val Gly Leu His
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7

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gaa tac ccg gta ggg tcg caa tta cct tgc gag ccc gaa ccg gac gtg    2784
Glu Tyr Pro Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp Val
        915                 920                 925

gcc gtg ttg acg tcc atg ctc act gat ccc tcc cat ata aca gca gag    2832
Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu
    930                 935                 940

gcg gcc ggg cga agg ttg gcg agg gga tca ccc ccc tct gtg gcc agc    2880
Ala Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Val Ala Ser
945                 950                 955                 960

tcc tcg gct agc cag cta tcc gct cca tct ctc aag gca act tgc acc    2928
Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr
                965                 970                 975

gct aac cat gac tcc cct gat gct gag ctc ata gag gcc aac ctc cta    2976
Ala Asn His Asp Ser Pro Asp Ala Glu Leu Ile Glu Ala Asn Leu Leu
            980                 985                 990

tgg agg cag gag atg ggc ggc aac atc acc agg gtt gag tca gaa aac    3024
Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu Asn
        995                 1000                1005

aaa gtg gtg att ctg gac tcc ttc gat ccg ctt gtg gcg gag gag gac    3072
Lys Val Val Ile Leu Asp Ser Phe Asp Pro Leu Val Ala Glu Glu Asp
    1010                1015                1020

gag cgg gag atc tcc gta ccc gca gaa atc ctg cgg aag tct cgg aga    3120
Glu Arg Glu Ile Ser Val Pro Ala Glu Ile Leu Arg Lys Ser Arg Arg
1025                1030                1035                1040

ttc gcc cag gcc ctg ccc gtt tgg gcg cgg ccg gac tat aac ccc ccg    3168
Phe Ala Gln Ala Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro
                1045                1050                1055

cta gtg gag acg tgg aaa aag ccc gac tac gaa cca cct gtg gtc cat    3216
Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His
            1060                1065                1070

ggc tgc ccg ctt cca cct cca aag tcc cct cct gtg cct ccg cct cgg    3264
Gly Cys Pro Leu Pro Pro Pro Lys Ser Pro Pro Val Pro Pro Pro Arg
        1075                1080                1085

aag aag cgg acg gtg gtc ctc act gaa tca acc cta tct act gcc ttg    3312
Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr Leu Ser Thr Ala Leu
    1090                1095                1100

gcc gag ctc gcc acc aga agc ttt ggc agc tcc tca act tcc ggc att    3360
Ala Glu Leu Ala Thr Arg Ser Phe Gly Ser Ser Ser Thr Ser Gly Ile
1105                1110                1115                1120

acg ggc gac aat acg aca aca tcc tct gag ccc gcc cct tct ggc tgc    3408
Thr Gly Asp Asn Thr Thr Thr Ser Ser Glu Pro Ala Pro Ser Gly Cys
            1125                1130                1135
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8

```
ccc ccc gac tcc gac gct gag tcc tat tcc tcc atg ccc ccc ctg gag    3456
Pro Pro Asp Ser Asp Ala Glu Ser Tyr Ser Ser Met Pro Pro Leu Glu
         1140                1145                1150

ggg gag cct ggg gat ccg gat ctt agc gac ggg tca tgg tca acg gtc    3504
Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser Trp Ser Thr Val
         1155                1160                1165

agt agt gag gcc aac gcg gag gat gtc gtg tgc tgc tca atg tct tac    3552
Ser Ser Glu Ala Asn Ala Glu Asp Val Val Cys Cys Ser Met Ser Tyr
      1170                1175                1180

tct tgg aca ggc gca ctc gtc acc ccg tgc gcc gcg gaa gaa cag aaa    3600
Ser Trp Thr Gly Ala Leu Val Thr Pro Cys Ala Ala Glu Glu Gln Lys
1185                1190                1195                1200

ctg ccc atc aat gca cta agc aac tcg ttg cta cgt cac cac aat ttg    3648
Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg His His Asn Leu
               1205                1210                1215

gtg tat tcc acc acc tca cgc agt gct tgc caa agg cag aag aaa gtc    3696
Val Tyr Ser Thr Thr Ser Arg Ser Ala Cys Gln Arg Gln Lys Lys Val
            1220                1225                1230

aca ttt gac aga ctg caa gtt ctg gac agc cat tac cag gac gta ctc    3744
Thr Phe Asp Arg Leu Gln Val Leu Asp Ser His Tyr Gln Asp Val Leu
         1235                1240                1245

aag gag gtt aaa gca gcg gcg tca aaa gtg aag gct aac ttg cta tcc    3792
Lys Glu Val Lys Ala Ala Ala Ser Lys Val Lys Ala Asn Leu Leu Ser
      1250                1255                1260

gta gag gaa gct tgc agc ctg acg ccc cca cac tca gcc aaa tcc aag    3840
Val Glu Glu Ala Cys Ser Leu Thr Pro Pro His Ser Ala Lys Ser Lys
1265                1270                1275                1280

ttt ggt tat ggg gca aaa gac gtc cgt tgc cat gcc aga aag gcc gta    3888
Phe Gly Tyr Gly Ala Lys Asp Val Arg Cys His Ala Arg Lys Ala Val
               1285                1290                1295

acc cac atc aac tcc gtg tgg aaa gac ctt ctg gaa gac aat gta aca    3936
Thr His Ile Asn Ser Val Trp Lys Asp Leu Leu Glu Asp Asn Val Thr
               1300                1305                1310

cca ata gac act acc atc atg gct aag aac gag gtt ttc tgc gtt cag    3984
Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Gln
         1315                1320                1325

cct gag aag ggg ggt cgt aag cca gct cgt ctc atc gtg ttc ccc gat    4032
Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile Val Phe Pro Asp
      1330                1335                1340

ctg ggc gtg cgc gtg tgc gaa aag atg gct ttg tac gac gtg gtt aca    4080
Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Val Val Thr
1345                1350                1355                1360
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9

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aag ctc ccc ttg gcc gtg atg gga agc tcc tac gga ttc caa tac tca      4128
Lys Leu Pro Leu Ala Val Met Gly Ser Ser Tyr Gly Phe Gln Tyr Ser
            1365                1370                1375

cca gga cag cgg gtt gaa ttc ctc gtg caa gcg tgg aag tcc aag aaa      4176
Pro Gly Gln Arg Val Glu Phe Leu Val Gln Ala Trp Lys Ser Lys Lys
            1380                1385                1390

acc cca atg ggg ttc tcg tat gat acc cgc tgc ttt gac tcc aca gtc      4224
Thr Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val
        1395                1400                1405

act gag agc gac atc cgt acg gag gag gca atc tac caa tgt tgt gac      4272
Thr Glu Ser Asp Ile Arg Thr Glu Glu Ala Ile Tyr Gln Cys Cys Asp
    1410                1415                1420

ctc gac ccc caa gcc cgc gtg gcc atc aag tcc ctc acc gag agg ctt      4320
Leu Asp Pro Gln Ala Arg Val Ala Ile Lys Ser Leu Thr Glu Arg Leu
1425                1430                1435                1440

tat gtt ggg ggc cct ctt acc aat tca agg ggg gag aac tgc ggc tat      4368
Tyr Val Gly Gly Pro Leu Thr Asn Ser Arg Gly Glu Asn Cys Gly Tyr
                1445                1450                1455

cgc agg tgc cgc gcg agc ggc gta ctg aca act agc tgt ggt aac acc      4416
Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys Gly Asn Thr
            1460                1465                1470

ctc act tgc tac atc aag gcc cgg gca gcc tgt cga gcc gca ggg ctc      4464
Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala Ala Gly Leu
        1475                1480                1485

cag gac tgc acc atg ctc gtg tgt ggc gac gac tta gtc gtt atc tgt      4512
Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val Val Ile Cys
    1490                1495                1500

gaa agc gcg ggg gtc cag gag gac gcg gcg agc ctg aga gcc ttc acg      4560
Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Leu Arg Ala Phe Thr
1505                1510                1515                1520

gag gct atg acc agg tac tcc gcc ccc cct ggg gac ccc cca caa cca      4608
Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro
                1525                1530                1535

gaa tac gac ttg gag ctc ata aca tca tgc tcc tcc aac gtg tca gtc      4656
Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val
                1540                1545                1550

gcc cac gac ggc gct gga aag agg gtc tac tac ctc acc cgt gac cct      4704
Ala His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro
        1555                1560                1565

aca acc ccc ctc gcg aga gct gcg tgg gag aca gca aga cac act cca      4752
Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro
    1570                1575                1580

gtc aat tcc tgg cta ggc aac ata atc atg ttt gcc ccc aca ctg tgg      4800
```

10

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Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe Ala Pro Thr Leu Trp
1585            1590            1595            1600

gcg agg atg ata ctg atg acc cat ttc ttt agc gtc ctt ata gcc agg    4848
Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Val Leu Ile Ala Arg
            1605            1610            1615

gac cag ctt gaa cag gcc ctc gat tgc gag atc tac ggg gcc tgc tac    4896
Asp Gln Leu Glu Gln Ala Leu Asp Cys Glu Ile Tyr Gly Ala Cys Tyr
        1620            1625            1630

tcc ata gaa cca ctg gat cta cct cca atc att caa aga ctc cat ggc    4944
Ser Ile Glu Pro Leu Asp Leu Pro Pro Ile Ile Gln Arg Leu His Gly
        1635            1640            1645

ctc agc gca ttt tca ctc cac agt tac tct cca ggt gaa atc aat agg    4992
Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly Glu Ile Asn Arg
    1650            1655            1660

gtg gcc gca tgc ctc aga aaa ctt ggg gta ccg ccc ttg cga gct tgg    5040
Val Ala Ala Cys Leu Arg Lys Leu Gly Val Pro Pro Leu Arg Ala Trp
1665            1670            1675            1680

aga cac cgg gcc cgg agc gtc cgc gct agg ctt ctg gcc aga gga ggc    5088
Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu Ala Arg Gly Gly
            1685            1690            1695

agg gct gcc ata tgt ggc aag tac ctc ttc aac tgg gca gta aga aca    5136
Arg Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn Trp Ala Val Arg Thr
        1700            1705            1710

aag ctc aaa ctc act cca ata gcg gcc gct ggc cag ctg gac ttg tcc    5184
Lys Leu Lys Leu Thr Pro Ile Ala Ala Ala Gly Gln Leu Asp Leu Ser
        1715            1720            1725

ggc tgg ttc acg gct ggc tac agc ggg gga gac att tat cac agc gtg    5232
Gly Trp Phe Thr Ala Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Val
    1730            1735            1740

tct cat gcc cgg ccc cgc tgg atc tgg ttt tgc cta ctc ctg ctt gct    5280
Ser His Ala Arg Pro Arg Trp Ile Trp Phe Cys Leu Leu Leu Leu Ala
1745            1750            1755            1760

gca ggg gta ggc atc tac ctc ctc ccc aac cga atg agc acg aat cct    5328
Ala Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg Met Ser Thr Asn Pro
            1765            1770            1775

aaa cct caa aga aag acc aaa cgt aac acc aac cgg cgg ccg cag gac    5376
Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp
            1780            1785            1790

gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg ttg    5424
Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu
        1795            1800            1805

ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg aga aag act tcc    5472
Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser
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gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gct cgt     5520
Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg
1825            1830                1835                1840

cgg ccc gag ggc agg acc tgg gct cag ccc ggg tac cct tgg ccc ctc     5568
Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu
                1845                1850                1855

tat ggc aat gag ggc tgc ggg tgg gcg gga tgg ctc ctg tct ccc cgt     5616
Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg
            1860                1865                1870

ggc tct cgg cct agc tgg ggc ccc aca gac ccc cgg cgt agg tcg cgc     5664
Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg
            1875                1880                1885

aat ttg ggt aag                                                     5676
Asn Leu Gly Lys
    1890
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<210> 6
<211> 1892
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of a representative modified fusion protein,
      with the NS3 protease domain deleted from the N-terminus and
      including amino acids 1-121 of Core on the C-terminus

<400> 6

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Met Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro
 1               5                  10                  15

Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His
            20                  25                  30

Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly
            35                  40                  45

Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly
    50                  55                  60

Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser
65                  70                  75                  80

Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala
                85                  90                  95

Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro
            100                 105                 110

Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser
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            115                     120                      125

Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val
    130             135             140

Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys
145             150             155             160

Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala
            165             170             175

Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val
            180             185             190

Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe
            195             200             205

Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe
    210             215             220

Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Ile Thr Leu Pro Gln Asp
225             230             235             240

Ala Val Ser Arg Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro
            245             250             255

Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe
            260             265             270

Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr
            275             280             285

Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn
    290             295             300

Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly
305             310             315             320

Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr
            325             330             335

Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu Val Ala Tyr Gln Ala Thr
            340             345             350

Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp
    355             360             365

Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu
    370             375             380

Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Ile Thr Leu Thr His Pro
385             390             395             400

Val Thr Lys Tyr Ile Met Thr Cys Met Ser Ala Asp Leu Glu Val Val
            405             410             415

Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala
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                        420                           425                         430

Tyr Cys Leu Ser Thr Gly Cys Val Val Ile Val Gly Arg Val Val Leu
        435                 440                 445

Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu
        450                 455                 460

Phe Asp Glu Met Glu Glu Cys Ser Gln His Leu Pro Tyr Ile Glu Gln
465                 470                 475                     480

Gly Met Met Leu Ala Glu Gln Phe Lys Gln Lys Ala Leu Gly Leu Leu
                485                 490                 495

Gln Thr Ala Ser Arg Gln Ala Glu Val Ile Ala Pro Ala Val Gln Thr
                500                 505                 510

Asn Trp Gln Lys Leu Glu Thr Phe Trp Ala Lys His Met Trp Asn Phe
        515                 520                 525

Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn
    530                 535                 540

Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ala Val Thr Ser Pro
545                 550                 555                     560

Leu Thr Thr Ser Gln Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val
                565                 570                 575

Ala Ala Gln Leu Ala Ala Pro Gly Ala Ala Thr Ala Phe Val Gly Ala
                580                 585                 590

Gly Leu Ala Gly Ala Ala Ile Gly Ser Val Gly Leu Gly Lys Val Leu
        595                 600                 605

Ile Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu Val
    610                 615                 620

Ala Phe Lys Ile Met Ser Gly Glu Val Pro Ser Thr Glu Asp Leu Val
625                 630                 635                     640

Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val
                645                 650                 655

Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala
                660                 665                 670

Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His
        675                 680                 685

Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val
        690                 695                 700

Thr Ala Ile Leu Ser Ser Leu Thr Val Thr Gln Leu Leu Arg Arg Leu
705                 710                 715                     720

His Gln Trp Ile Ser Ser Glu Cys Thr Thr Pro Cys Ser Gly Ser Trp
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Leu Arg Asp Ile Trp Asp Trp Ile Cys Glu Val Leu Ser Asp Phe Lys
          740   745   750

Thr Trp Leu Lys Ala Lys Leu Met Pro Gln Leu Pro Gly Ile Pro Phe
      755   760   765

Val Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile
      770   775   780

Met His Thr Arg Cys His Cys Gly Ala Glu Ile Thr Gly His Val Lys
785   790   795   800

Asn Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg Asn Met Trp
          805   810   815

Ser Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro
        820   825   830

Leu Pro Ala Pro Asn Tyr Thr Phe Ala Leu Trp Arg Val Ser Ala Glu
      835   840   845

Glu Tyr Val Glu Ile Arg Gln Val Gly Asp Phe His Tyr Val Thr Gly
      850   855   860

Met Thr Thr Asp Asn Leu Lys Cys Pro Cys Gln Val Pro Ser Pro Glu
865   870   875   880

Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Phe Ala Pro Pro
          885   890   895

Cys Lys Pro Leu Leu Arg Glu Glu Val Ser Phe Arg Val Gly Leu His
        900   905   910

Glu Tyr Pro Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp Val
        915   920   925

Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu
      930   935   940

Ala Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Val Ala Ser
945   950   955   960

Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr
        965   970   975

Ala Asn His Asp Ser Pro Asp Ala Glu Leu Ile Glu Ala Asn Leu Leu
        980   985   990

Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu Asn
        995   1000   1005

Lys Val Val Ile Leu Asp Ser Phe Asp Pro Leu Val Ala Glu Glu Asp
      1010   1015   1020

Glu Arg Glu Ile Ser Val Pro Ala Glu Ile Leu Arg Lys Ser Arg Arg

15

Phe Ala Gln Ala Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro
                1045   1050   1055

Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His
            1060   1065   1070

Gly Cys Pro Leu Pro Pro Pro Lys Ser Pro Pro Val Pro Pro Pro Arg
           1075   1080   1085

Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr Leu Ser Thr Ala Leu
          1090   1095   1100

Ala Glu Leu Ala Thr Arg Ser Phe Gly Ser Ser Ser Thr Ser Gly Ile
1105   1110   1115   1120

Thr Gly Asp Asn Thr Thr Thr Ser Ser Glu Pro Ala Pro Ser Gly Cys
                1125   1130   1135

Pro Pro Asp Ser Asp Ala Glu Ser Tyr Ser Ser Met Pro Pro Leu Glu
                1140   1145   1150

Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser Trp Ser Thr Val
           1155   1160   1165

Ser Ser Glu Ala Asn Ala Glu Asp Val Val Cys Cys Ser Met Ser Tyr
          1170   1175   1180

Ser Trp Thr Gly Ala Leu Val Thr Pro Cys Ala Ala Glu Glu Gln Lys
1185   1190   1195   1200

Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg His His Asn Leu
                1205   1210   1215

Val Tyr Ser Thr Thr Ser Arg Ser Ala Cys Gln Arg Gln Lys Lys Val
           1220   1225   1230

Thr Phe Asp Arg Leu Gln Val Leu Asp Ser His Tyr Gln Asp Val Leu
           1235   1240   1245

Lys Glu Val Lys Ala Ala Ala Ser Lys Val Lys Ala Asn Leu Leu Ser
          1250   1255   1260

Val Glu Glu Ala Cys Ser Leu Thr Pro Pro His Ser Ala Lys Ser Lys
1265   1270   1275   1280

Phe Gly Tyr Gly Ala Lys Asp Val Arg Cys His Ala Arg Lys Ala Val
                1285   1290   1295

Thr His Ile Asn Ser Val Trp Lys Asp Leu Leu Glu Asp Asn Val Thr
                1300   1305   1310

Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Gln
           1315   1320   1325

Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile Val Phe Pro Asp

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     1330                    1335                    1340

Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Val Val Thr
1345                    1350                    1355                    1360

Lys Leu Pro Leu Ala Val Met Gly Ser Ser Tyr Gly Phe Gln Tyr Ser
               1365                    1370                    1375

Pro Gly Gln Arg Val Glu Phe Leu Val Gln Ala Trp Lys Ser Lys Lys
          1380                    1385                    1390

Thr Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val
          1395                    1400                    1405

Thr Glu Ser Asp Ile Arg Thr Glu Glu Ala Ile Tyr Gln Cys Cys Asp
      1410                    1415                    1420

Leu Asp Pro Gln Ala Arg Val Ala Ile Lys Ser Leu Thr Glu Arg Leu
1425                    1430                    1435                    1440

Tyr Val Gly Gly Pro Leu Thr Asn Ser Arg Gly Glu Asn Cys Gly Tyr
               1445                    1450                    1455

Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys Gly Asn Thr
          1460                    1465                    1470

Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala Ala Gly Leu
          1475                    1480                    1485

Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val Val Ile Cys
      1490                    1495                    1500

Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Leu Arg Ala Phe Thr
1505                    1510                    1515                    1520

Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro
               1525                    1530                    1535

Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val
          1540                    1545                    1550

Ala His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro
          1555                    1560                    1565

Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro
      1570                    1575                    1580

Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe Ala Pro Thr Leu Trp
1585                    1590                    1595                    1600

Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Val Leu Ile Ala Arg
               1605                    1610                    1615

Asp Gln Leu Glu Gln Ala Leu Asp Cys Glu Ile Tyr Gly Ala Cys Tyr
          1620                    1625                    1630

Ser Ile Glu Pro Leu Asp Leu Pro Pro Ile Ile Gln Arg Leu His Gly
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Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly Glu Ile Asn Arg
   1650   1655   1660

Val Ala Ala Cys Leu Arg Lys Leu Gly Val Pro Pro Leu Arg Ala Trp
1665   1670   1675   1680

Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu Ala Arg Gly Gly
         1685   1690   1695

Arg Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn Trp Ala Val Arg Thr
      1700   1705   1710

Lys Leu Lys Leu Thr Pro Ile Ala Ala Ala Gly Gln Leu Asp Leu Ser
     1715   1720   1725

Gly Trp Phe Thr Ala Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Val
    1730   1735   1740

Ser His Ala Arg Pro Arg Trp Ile Trp Phe Cys Leu Leu Leu Leu Ala
1745   1750   1755   1760

Ala Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg Met Ser Thr Asn Pro
        1765   1770   1775

Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp
        1780   1785   1790

Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu
      1795   1800   1805

Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser
   1810   1815   1820

Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg
1825   1830   1835   1840

Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu
      1845   1850   1855

Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg
        1860   1865   1870

Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg
     1875   1880   1885

Asn Leu Gly Lys
   1890

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<211> 21
<212> PRT
<213> Artificial

<220>

18

<223> E2 epitope consensus sequence

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Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro
1   5   10   15

Gly Ala Lys Gln Asn
            20

<210> 8
<211> 23
<212> PRT
<213> Artificial

<220>
<223> NS4A peptide

<400> 8

Lys Lys Gly Ser Val Val Ile Val Gly Arg Ile Val Leu Ser Gly Lys
1   5   10   15

Pro Ala Ile Ile Pro Lys Lys
            20